

WEST Search History

DATE: Tuesday, July 30, 2002

Set Name Query side by side		Hit Count	Set Name result set	
DB=USPT,DWPI; PLUR=YES; OP=ADJ				
L49	L48 not 147	27	L49	
L48	differential expression and (13 or 14 or 16 or 17 or 18 or 19 or 110 or 111 or 112 or 113 or 114 or 115 or 116 or 117 or 118 or 119 or 120 or 121 or 122 or 123)	35	L48	
L47	differential display and (13 or 14 or 16 or 17 or 18 or 19 or 110 or 111 or 112 or 113 or 114 or 115 or 116 or 117 or 118 or 119 or 120 or 121 or 122 or 123)	20	L47	
L46	gaddis-s\$.in.	6	L46	
L45	gaddis-s\$.in. and combinatorial oligonucleotide per	. 0	L45	
L44	12 same (multiple or several)	33	L44	
L43	L1 and 124	0	L43	
L42	L1 and 123	4	L42	
L41	L1 and 122	1	L41	
L40	L1 and 121	1	L40	
L39	L1 and 120	0	L39	
L38	11 and 119	1	L38	
L37	11 and 117	0	L37	
L36	11 and 116	0	L36	
L35	11 and 115	0	L35	
L34	11 and 114	0	L34	
L33	11 and 113	3	L33	
L32	11 and 112	1	L32	
L31	11 and 110	0	L31	
L30	11 and 19	1	L30	
L29	11 and 18	1	L29	
L28	11 and 17	2	L28	
L27	11 and 16	3	L27	
L26	11 and 14	0	L26	
L25	11 and 13	1	L25	
L24	vdac1 or vdac 1 or voltage dependent anion channel 1	6	L24	
L23	vacuolar n\$1 atpase or (atpase near3 (vacuolar or "v"))	117	L23	
L22	(atp citrate near3 lyase) or atp dependent citrate lyase or citrate cleavage enzyme	64	L22	
L21	(na k atpase or sodium potassium atpase) near5 (beta\$1 near3 subunit)	7	L21	
L20	coupling factor 6 or (atpase near3 (f6 or f 6))	7	L20	
L19	113 near10 (beta near3 subunit)	29	L19	



L18	117 and 1 type	2	L18
L17	113 near10 (gamma near3 subunit)	8	L17
L16	ac45	8	L16
L15	113 near10 (alpha near3 subunit)	23	L15
L14	113 near10 ("c" near3 subunit)	21	L14
L13	atp synthase	172	L13
L12	mcl1 or myeloid cell factor 1 or myeloid cell differentiation protein	41	L12
L11	cofilin near10 non muscle	5	L11
L10	cofilin	29	L10
L9	myosin regulatory light chain or (myosin light chain near5 regulator\$3)	19	L9
L8	adducin near5 gamma	2	L8
L7	actin depolymeri\$8 or adf or actin capping or actin filament capping	2502	L7
L6	prothymosin alpha\$1	37	L6
L5	prothymosin alpha	37	L5
L4	thymosin near3 (beta4 or beta 4)	29	L4
L3	profilin	66	L3
L2	L1 same control	363	L2
L1	(housekeeping or maintenance)near5 gene	1413	L1

END OF SEARCH HISTORY

(FILE 'HOME' ENTERED AT 09:01:09 ON 30 JUL 2002)

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FILE 'MEDLINE, LIFESCI, SCISEARCH, EMBASE, BIOSIS, CAPLUS' ENTERED AT
     09:02:26 ON 30 JUL 2002
          15742 S (HOUSEKEEPING OR MAINTENANCE) (10A) GENE#
Ъ1
           2468 S L1(P)(CONTROL OR STANDARD)
L2
L3
           4267 S PROFILIN
           1684 S (THYMOSIN(3A) (BETA4 OR BETA 4))
L4
L_5
           1431 S PROTHYMOSIN ALPHA#
           9429 S ACTIN DEPOLYMERI######## OR ADF OR ACTIN CAPPING OR ACTIN FI
L6
             82 S ADDUCIN (5A) GAMMA
L7
           3244 S MYOSIN REGULATORY LIGHT CHAIN# OR (MYOSIN LIGHT CHAIN(5A) REGU
L8
           1902 S COFILIN
Ъ9
L10
             32 S COFILIN(10A)(NON MUSCLE)
            432 S MCL1 OR MYELOID CELL FACTOR 1 OR MYELOID CELL DIFFERENTIATION
L11
L12
          12931 S ATP SYNTHASE
           1010 S L12(10A)("C"(3A)SUBUNIT)
L13
T.14
            524 S L12 (10A) (ALPHA (3A) SUBUNIT)
              1 S L12(P)AC45
L15
             43 S AC45
            440 S L12 (10A) (GAMMA (3A) SUBUNIT)
L17
L18
              7 S L17 AND L TYPE
L19
           1010 S L12(10A) (BETA(3A) SUBUNIT)
L20
            177 S COUPLING FACTOR 6 OR (ATPASE(3A) (F6 OR F 6))
           1890 S (NA K ATPASE OR SODIUM POTASSIUM ATPASE) (5A) (BETA#(3A) SUBUNIT
L21
           3599 S (ATP CITRATE(3A)LYASE) OR ATP DEPENDENT CITRATE LYASE OR CITR
L22
        2443453 S VACUOLAR H# ATPASE OR (ATPASE(3A)VACUOLAR OR "V")
T<sub>1</sub>2.3
L24
           9403 S VACUOLAR H# ATPASE OR (ATPASE(3A)(VACUOLAR OR "V"))
            870 S AQP3 OR AQUAPORIN# 3
            178 S VDAC1 OR VDAC 1 OR VOLTAGE DEPENDENT ANION CHANNEL 1
L26
              6 S L1 AND L3
T<sub>2</sub>7
L28
              3 S L1 AND L4
              2 DUP REM L27 (4 DUPLICATES REMOVED)
L29
              1 DUP REM L28 (2 DUPLICATES REMOVED)
L30
              5 S L1 AND L5
L31
              5 DUP REM L31 (0 DUPLICATES REMOVED)
L32
L33
              3 S L1 AND L6
L34
              3 DUP REM L33 (0 DUPLICATES REMOVED)
L35
              0 S L1 AND L7
              1 S L1 AND L8
L36
L37
              1 S L1 AND L9
              0 S L1 AND L10
L38
L39
              2 S L1 AND L11
              1 DUP REM L39 (1 DUPLICATE REMOVED)
L40
             37 S L1 AND L12
L41
             16 DUP REM L41 (21 DUPLICATES REMOVED)
L42
L43
              1 S L1 AND L13
              2 S L1 AND L14
L44
L45
              2 DUP REM L44 (0 DUPLICATES REMOVED)
L46
              0 S L1 AND L16
              1 S L1 AND L17
L47
L48
              0 S L1 AND L18
              8 S L1 AND L19
L49
              3 DUP REM L49 (5 DUPLICATES REMOVED)
T<sub>2</sub>50
L51
              1 S L1 AND L20
L52
              0 S L1 AND L21
              1 S L1 AND L22
L53
             13 S L1 AND L24
L54
              5 DUP REM L54 (8 DUPLICATES REMOVED)
L55
              1 S L1 AND L25
L56
              6 S L1 AND L26
L57
              1 DUP REM L57 (5 DUPLICATES REMOVED)
L58
              5 S L42 AND (L29 OR L30 OR L32 OR L34 OR L36 OR L37 OR L4
L59
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L60 443 S (L3 OR L4 OR L5 OR L6 OR L7 OR L8 OR L9 OR L10 OR L11 L61 215 DUP REM L60 (228 DUPLICATES REMOVED)
L62 160 S L61 NOT (2001-2002/PY)

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